OIPE

```
          RAW SEQUENCE LISTING             DATE: 02/08/2001
          PATENT APPLICATION:  US/09/771,045    TIME: 12:14:08

          Input Set : A:\1134CSEQLIST.TXT
          Output Set: N:\CRF3\02082001\I771045.raw
```

Does Not Comply Corrected Diskette Needed

P 6

```
     4 <110> APPLICANT: Duvick, Jonathan P.
     5         Gilliam, Jacob T.
     6         Maddox, Joyce R.
     8 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
     9         Polynucleotides and Related Polypeptides and Methods of Use
    12 <130> FILE REFERENCE: 1134C
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/771,045
C--> 14 <141> CURRENT FILING DATE: 2001-01-26
    14 <150> PRIOR APPLICATION NUMBER: US 60/092,936
    15 <151> PRIOR FILING DATE: 1998-07-15
    17 <150> PRIOR APPLICATION NUMBER: US 60/135,391
    18 <151> PRIOR FILING DATE: 1999-05-21
    20 <150> PRIOR APPLICATION NUMBER: US 09/352,159
    21 <151> PRIOR FILING DATE: 1999-07-12
    23 <150> PRIOR APPLICATION NUMBER: US 09/352,168
    24 <151> PRIOR FILING DATE: 1999-07-12
    26 <160> NUMBER OF SEQ ID NOS: 53
    28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
    30 <210> SEQ ID NO: 1
    31 <211> LENGTH: 372
    32 <212> TYPE: DNA
    33 <213> ORGANISM: Exophiala spinifera
    35 <220> FEATURE:
    36 <221> NAME/KEY: misc_feature
    37 <222> LOCATION: (346)...(346)
    38 <223> OTHER INFORMATION: n = A,T,C or G
    40 <400> SEQUENCE: 1
    41  gggccccggc gttctcgtag gctgcgcgga gttggtccca gacagacttt tgtcgtacct      60
    42  gcttggactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc     120
    43  attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt     180
    44  ggaggacgcc cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct     240
    45  tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg     300
    46  gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc     360
    47  ggaacacggc gc                                                        372
    49 <210> SEQ ID NO: 2
    50 <211> LENGTH: 182
    51 <212> TYPE: DNA
    52 <213> ORGANISM: Exophiala spinifera
    54 <400> SEQUENCE: 2
    55  gaattttccg ccaatgcttg cttctcggcg ggaagaggtg gtgaaaatgt caaggtggga      60
    56  tacaaggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc     120
    57  gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc     180
    58  ac                                                                   182
    60 <210> SEQ ID NO: 3
    61 <211> LENGTH: 29
    62 <212> TYPE: DNA
    63 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING   DATE: 02/08/2001
PATENT APPLICATION: US/09/771,045   TIME: 12:14:08

Input Set : A:\1134CSEQLIST.TXT
Output Set: N:\CRF3\02082001\I771045.raw

```
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965
69 <400> SEQUENCE: 3
70  tggtttcgtt accgacaacc ttgtatccc                                    29
72 <210> SEQ ID NO: 4
73 <211> LENGTH: 28
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Designed oligonucleotide for 5' RACE, 21968
80 <400> SEQUENCE: 4
81  gagttggtcc cagacagact tttgtcgt                                     28
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 1389
85 <212> TYPE: DNA
86 <213> ORGANISM: Exophiala spinifera
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (1)...(1386)
92 <400> SEQUENCE: 5
93  gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg   48
94  Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
95  1               5                   10                  15
97  gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt   96
98  Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
99              20                  25                  30
101 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt  144
102 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
103             35                  40                  45
105 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac  192
106 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
107     50                  55                  60
109 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag  240
110 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
111 65                  70                  75                  80
113 ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac  288
114 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
115             85                  90                  95
117 ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag  336
118 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
119             100                 105                 110
121 gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc  384
122 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
123             115                 120                 125
125 gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg  432
126 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
127     130                 135                 140
129 ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg  480
130 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
```

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131  145               150               155               160
133  cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt      528
134  Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
135                165               170               175
137  gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag      576
138  Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
139                180               185               190
141  agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg      624
142  Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
143                195               200               205
145  cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg      672
146  Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
147      210               215               220
149  tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct      720
150  Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
151  225               230               235               240
153  gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc      768
154  Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
155                245               250               255
157  gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg      816
158  Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
159                260               265               270
161  tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca      864
162  Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
163                275               280               285
165  ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta      912
166  Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
167      290               295               300
169  tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa      960
170  Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
171  305               310               315               320
173  tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc     1008
174  Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
175                325               330               335
177  gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg     1056
178  Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
179                340               345               350
181  aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac     1104
182  Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
183      355               360               365
185  caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg     1152
186  Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
187      370               375               380
189  gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga     1200
190  Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
191  385               390               395               400
193  gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg     1248
194  Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
195                405               410               415
```

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197  gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg      1296
198  Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
199              420                 425                 430
201  tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa      1344
202  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
203              435                 440                 445
205  cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca              1386
206  Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
207      450                 455                 460
209  tag                                                                  1389
211  <210> SEQ ID NO: 6
212  <211> LENGTH: 462
213  <212> TYPE: PRT
214  <213> ORGANISM: Exophiala spinifera
216  <400> SEQUENCE: 6
217  Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
218  1               5                   10                  15
219  Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
220              20                  25                  30
221  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
222              35                  40                  45
223  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
224      50                  55                  60
225  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
226  65                  70                  75                  80
227  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
228              85                  90                  95
229  Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
230              100                 105                 110
231  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
232              115                 120                 125
233  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
234      130                 135                 140
235  Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
236  145                 150                 155                 160
237  Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
238              165                 170                 175
239  Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
240              180                 185                 190
241  Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
242              195                 200                 205
243  Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
244      210                 215                 220
245  Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
246  225                 230                 235                 240
247  Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
248              245                 250                 255
249  Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
250              260                 265                 270
```

Input Set : A:\1134CSEQLIST.TXT
Output Set: N:\CRF3\02082001\I771045.raw

```
251  Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
252          275              280              285
253  Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
254          290              295          -       300
255  Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
256  305              310              315                  320
257  Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
258              325              330              335
259  Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
260          340              345              350
261  Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
262          355              360              365
263  Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
264          370              375              380
265  Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
266  385              390              395                  400
267  Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
268              405              410              415
269  Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
270          420              425              430
271  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
272          435              440              445
273  Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
274          450              455              460
276  <210> SEQ ID NO: 7
277  <211> LENGTH: 1442
278  <212> TYPE: DNA
279  <213> ORGANISM: Exophiala spinifera
281  <220> FEATURE:
282  <221> NAME/KEY: CDS
283  <222> LOCATION: (1)...(646)
285  <221> NAME/KEY: intron
286  <222> LOCATION: (647)...(699)
288  <221> NAME/KEY: CDS
289  <222> LOCATION: (700)...(1439)
291  <400> SEQUENCE: 7
292  gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg      48
293  Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
294  1               5                   10                  15
296  gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
297  Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
298              20                  25                  30
300  gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt     144
301  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
302          35                  40                  45
304  ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac     192
305  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
306          50                  55                  60
308  agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag     240
```

```
<210> 19
  <211> 692
  <212> PRT
  <213> Unknown
  <400> 19
```
see item 12 on Error Summary Sheet

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

FYI.

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
VERIFICATION SUMMARY                    DATE: 02/08/2001
PATENT APPLICATION:  US/09/771,045      TIME: 12:14:09

          Input Set : A:\1134CSEQLIST.TXT
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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:349 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:1234 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1234 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1334 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1335 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1488 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2095 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2517 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2989 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2989 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:3153 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3154 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3487 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:3487 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:3810 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:3810 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:4247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
```

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION   SERIAL NUMBER: _09/177,045_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

19 and more

12 ✓ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

BIOTECHNOLOGY
SYSTEMS
BRANCH
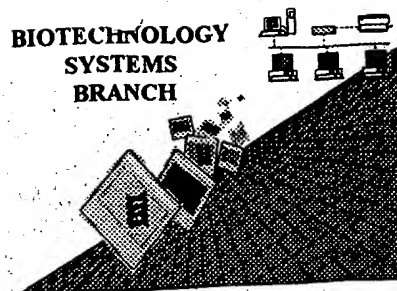
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/771,045_

Source: _OIPE_

Date Processed by STIC: _2/8/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker